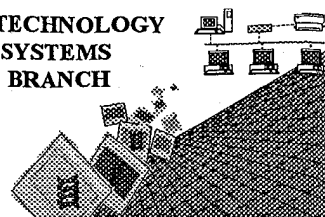BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 09/695,369
Source: OIPE,
Date Processed by STIC: 2/12/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**
          http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
              Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/695,369_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _16, 21_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

P 6

```
 3 <110> APPLICANT: Xu, Wenfeng
 4        Lofton-Day, Catherine E.
 5        Henne, Randall
 6        Presnell, Scott R.
 7        Yao, Yue
 8        Novak, Julia E.
 9        Foster, Donald C.
10        Yee, David P.
12 <120> TITLE OF INVENTION: UMLR POLYPEPTIDES
14 <130> FILE REFERENCE: 99-75
16 <140> CURRENT APPLICATION NUMBER: US/09/695,369
16 <141> CURRENT FILING DATE: 2002-01-24
16 <150> PRIOR APPLICATION NUMBER: US 60/160,880
17 <151> PRIOR FILING DATE: 1999-10-22
19 <150> PRIOR APPLICATION NUMBER: US 60/163,215
20 <151> PRIOR FILING DATE: 1999-11-02
22 <150> PRIOR APPLICATION NUMBER: US 60/218,769
23 <151> PRIOR FILING DATE: 2000-07-17
25 <150> PRIOR APPLICATION NUMBER: US 60/222,221
26 <151> PRIOR FILING DATE: 2000-08-01
28 <160> NUMBER OF SEQ ID NOS: 50
30 <170> SOFTWARE: FastSEQ for Windows Version 3.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1162
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (104)...(913)
41 <400> SEQUENCE: 1
42   gaggggctg ggtgagatgt gtgctctgcg ctgaggtgga tttgtaccgg agtcccattt     60
43   gggagcaaga gccatctact cgtccgttac cggccttccc acc atg gat tgc caa    115
44                                                   Met Asp Cys Gln
45                                                    1
47   gaa aat gag tac tgg gac caa tgg gga cgg tgt gtc acc tgc caa cgg    163
48   Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val Thr Cys Gln Arg
49    5                  10                  15                  20
51   tgt ggt cct gga cag gag cta tcc aag gat tgt ggt tat gga gag ggt    211
52   Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly Tyr Gly Glu Gly
53                   25                  30                  35
55   gga gat gcc tac tgc aca gcc tgc cct cct cgc agg tac aaa agc agc    259
56   Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg Tyr Lys Ser Ser
57                   40                  45                  50
```

RAW SEQUENCE LISTING   DATE: 02/12/2002
PATENT APPLICATION: US/09/695,369   TIME: 13:22:39

Input Set : A:\99-75 SEQ.txt
Output Set: N:\CRF3\02122002\I695369.raw

```
59   tgg ggc cac cac aaa tgt cag agt tgc atc acc tgt gct gtc atc aat     307
60   Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys Ala Val Ile Asn
61           55                  60                  65
63   cgt gtt cag aag gtc aac tgc aca gct acc tct aat gct gtc tgt ggg     355
64   Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn Ala Val Cys Gly
65           70                  75                  80
67   gac tgt ttg ccc agg ttc tac cga aag aca cgc att gga ggc ctg cag     403
68   Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile Gly Gly Leu Gln
69    85                  90                  95                 100
71   gac caa gag tgc atc ccg tgc acg aag cag acc ccc acc tct gag gtt     451
72   Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro Thr Ser Glu Val
73               105                 110                 115
75   caa tgt gcc ttc cag ttg agc tta gtg gag gca gat gca ccc aca gtg     499
76   Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala Pro Thr Val
77               120                 125                 130
79   ccc cct cag gag gcc aca ctt gtt gca ctg gtg agc agc ctg cta gtg     547
80   Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser Leu Leu Val
81           135                 140                 145
83   gtg ttt acc ctg gcc ttc ctg ggg ctc ttc ttc ctc tac tgc aag cag     595
84   Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr Cys Lys Gln
85        150                 155                 160
87   ttc ttc aac aga cat tgc cag cgt gga ggt ttg ctg cag ttt gag gct     643
88   Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu Gln Phe Glu Ala
89   165                 170                 175                 180
91   gat aaa aca gca aag gag gaa tct ctc ttc ccc gtg cca ccc agc aag     691
92   Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val Pro Pro Ser Lys
93               185                 190                 195
95   gag acc agt gct gag tcc caa gag tcc ttt acc atg gcc tcc tgc acc     739
96   Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
97               200                 205                 210
99   tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca gag     787
100  Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
101          215                 220                 225
103  ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct gag     835
104  Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
105      230                 235                 240
107  acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg gag ctc     883
108  Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
109  245                 250                 255                 260
111  aat gtg ccc ttt gaa gtt ccc agc cct taa ctctaatgag gtctcttggg     933
112  Asn Val Pro Phe Glu Val Pro Ser Pro  *
113                      265
115  cccctggcag ccttgcccag ttgttctctc tggactctgt tcctatacca caacagcagc     993
116  aggggcctga aatgtgatgt ccacaagagc taatcccta cagatggggc atatcctatc     1053
117  ccatcccacc agaggattga ttctccattt cacaaggact gatctggagc atttcttgct     1113
118  tccctgttgt agtctgggga gccagattcc acatgcatgg ggcggccgc     1162
120  <210> SEQ ID NO: 2
121  <211> LENGTH: 269
122  <212> TYPE: PRT
```

```
123 <213> ORGANISM: Homo sapiens
125 <400> SEQUENCE: 2
126  Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
127   1               5                  10                  15
129  Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
130              20                  25                  30
131  Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
132          35                  40                  45
133  Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
134      50                  55                  60
135  Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
136  65                  70                  75                  80
137  Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
138              85                  90                  95
139  Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
140              100                 105                 110
141  Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
142          115                 120                 125
143  Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
144      130                 135                 140
145  Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
146  145                 150                 155                 160
147  Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
148              165                 170                 175
149  Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
150              180                 185                 190
151  Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met
152          195                 200                 205
153  Ala Ser Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile
154      210                 215                 220
155  Glu Cys Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr
156  225                 230                 235                 240
157  Thr Gly Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp
158              245                 250                 255
159  Arg Leu Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
160              260                 265
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 807
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: degenerate sequence
170 <221> NAME/KEY: misc_feature
171 <222> LOCATION: (1)...(807)
172 <223> OTHER INFORMATION: n = A,T,C or G
174 <400> SEQUENCE: 3
175  atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn    60
176  tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay   120
177  tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn   180
```

```
W--> 178    tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay    240
W--> 179    gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar    300
W--> 180    gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty    360
W--> 181    carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn    420
W--> 182    gcnytngtnw snwsnytnyt ngtngtntty acnytngcnt tyytnggnyt nttyttyytn    480
W--> 183    taytgyaarc arttyttyaa ymgncaytgy carmgnggng gnytnytnca rttygargcn    540
W--> 184    gayaaracng cnaargarga rwsnytntty ccngtnccnc cnwsnaarga racnwsngcn    600
W--> 185    garwsncarg arwsnttyac natggcnwsn tgyacnwsng arwsncayws ncaytgggtn    660
W--> 186    caywsnccna thgartgyac ngarytngay ytncaraart tywsnwsnws ngcnwsntay    720
W--> 187    acnggngcng aracnytngg nggnaayacn gtngarwsna cnggngaymg nytngarytn    780
W--> 188    aaygtnccnt tygargtncc nwsnccn                                        807
       190  <210> SEQ ID NO: 4
       191  <211> LENGTH: 41
       192  <212> TYPE: PRT
       193  <213> ORGANISM: Artificial Sequence
       195  <220> FEATURE:
       196  <223> OTHER INFORMATION: Pseudo repeat motif #1
       198  <221> NAME/KEY: VARIANT
       199  <222> LOCATION: (1)...(1)
       200  <223> OTHER INFORMATION: Xaa is any amino acid residue
       202  <221> NAME/KEY: VARIANT
       203  <222> LOCATION: (3)...(12)
       204  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       206  <221> NAME/KEY: VARIANT
       207  <222> LOCATION: (13)...(16)
       208  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       209        or not present
       211  <221> NAME/KEY: VARIANT
       212  <222> LOCATION: (19)...(20)
       213  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       215  <221> NAME/KEY: VARIANT
       216  <222> LOCATION: (22)...(26)
       217  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       219  <221> NAME/KEY: VARIANT
       220  <222> LOCATION: (27)...(30)
       221  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       222        or not present
       224  <221> NAME/KEY: VARIANT
       225  <222> LOCATION: (32)...(37)
       226  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       227        or not present
       229  <221> NAME/KEY: VARIANT
       230  <222> LOCATION: (38)...(39)
       231  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
       232        or not present
       234  <221> NAME/KEY: VARIANT
       235  <222> LOCATION: (41)...(41)
       236  <223> OTHER INFORMATION: Xaa is any amino acid residue
       238  <400> SEQUENCE: 4
```

RAW SEQUENCE LISTING   DATE: 02/12/2002
PATENT APPLICATION: US/09/695,369   TIME: 13:22:39

Input Set : A:\99-75 SEQ.txt
Output Set: N:\CRF3\02122002\I695369.raw

```
W--> 239  Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     240  1               5                   10                  15
W--> 241  Cys Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
     242              20                  25                  30
W--> 243  Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
     244          35                  40
     246  <210> SEQ ID NO: 5
     247  <211> LENGTH: 45
     248  <212> TYPE: PRT
     249  <213> ORGANISM: Artificial Sequence
     251  <220> FEATURE:
     252  <223> OTHER INFORMATION: Pseudo repeat motif #2
     254  <221> NAME/KEY: VARIANT
     255  <222> LOCATION: (1)...(1)
     256  <223> OTHER INFORMATION: Xaa is any amino acid residue
     258  <221> NAME/KEY: VARIANT
     259  <222> LOCATION: (3)...(15)
     260  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     262  <221> NAME/KEY: VARIANT
     263  <222> LOCATION: (16)...(17)
     264  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     265        or not present
     267  <221> NAME/KEY: VARIANT
     268  <222> LOCATION: (19)...(20)
     269  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     271  <221> NAME/KEY: VARIANT
     272  <222> LOCATION: (22)...(23)
     273  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     275  <221> NAME/KEY: VARIANT
     276  <222> LOCATION: (24)...(24)
     277  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     278        or not present
     280  <221> NAME/KEY: VARIANT
     281  <222> LOCATION: (26)...(33)
     282  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     284  <221> NAME/KEY: VARIANT
     285  <222> LOCATION: (34)...(36)
     286  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     287        or not present
     289  <221> NAME/KEY: VARIANT
     290  <222> LOCATION: (38)...(44)
     291  <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
     293  <400> SEQUENCE: 5
W--> 294  Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     295  1               5                   10                  15
W--> 296  Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     297              20                  25                  30
W--> 298  Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
     299          35                  40                  45
```

```
<210> SEQ ID NO 16
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220>
<223>
<400> SEQUENCE: 16
      Glu Tyr Met Pro Met Glu
      1               5
```

see item 11 on Error Summary Sheet

same error in Sequence 21

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Input Set : A:\99-75 SEQ.txt
Output Set: N:\CRF3\02122002\I695369.raw

```
L:16  M:270 C: Current Application Number differs, Replaced Current Application No
L:16  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:616 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:618 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:618 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:682 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:684 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:684 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
```

VERIFICATION SUMMARY   DATE: 02/12/2002
PATENT APPLICATION: US/09/695,369   TIME: 13:22:40

Input Set : **A:\99-75 SEQ.txt**
Output Set: **N:\CRF3\02122002\I695369.raw**

```
L:837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:900 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
```